

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/603,566A
Source: TFW16
Date Processed by STIC: 3-30-05

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 03/30/2005
PATENT APPLICATION: US/10/603,566A **TIME:** 10:56:07

Input Set : A:\March\~1.txt
Output Set: N:\CRF4\03302005\J603566A.raw

3 <110> APPLICANT: Wittamer, Valerie
4 Communi, David
5 Vandenbogaerde, Ann
6 Detheux, Michel
7 Parmentier, Marc
9 <120> TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
11 <130> FILE REFERENCE: 9409/2045B
13 <140> CURRENT APPLICATION NUMBER: 10/603,566A
14 <141> CURRENT FILING DATE: 2003-06-25
16 <150> PRIOR APPLICATION NUMBER: US 60/303,858
17 <151> PRIOR FILING DATE: 2001-07-09
19 <150> PRIOR APPLICATION NUMBER: US 09/905,253
20 <151> PRIOR FILING DATE: 2001-07-13
22 <150> PRIOR APPLICATION NUMBER: US 10/201,187
23 <151> PRIOR FILING DATE: 2001-07-23
25 <150> PRIOR APPLICATION NUMBER: PCT/EP02/07647
26 <151> PRIOR FILING DATE: 2002-07-09
28 <160> NUMBER OF SEQ ID NOS: 94
30 <170> SOFTWARE: PatentIn version 3.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1112
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <400> SEQUENCE: 1
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40 gactccattg tgggttttggaa ggacttatcc cccttggaaag ccagggtgac caggatcttc 120
42 ctgggtgtgg tctacagcat cgtctgcattc ctcgggattc tgggcaatgg tctgggtgatc 180
44 atcattgccca ccttcaagat gaagaagaca gtgaacatgg tctgggttctt caacctggca 240
46 gtggcagatt tcctgttcaa cgtcttccttc ccaatccata tcaccttatgc cgccatggac 300
48 taccactggg ttttcgggac accatgtgc aagatcagca acttccttct catccacaac 360
50 atgttccacca gcgtcttcctt gctgaccatc atcagacttg accgctgcattt ctctgtgctc 420
52 ctccctgtctt ggtcccgagaa ccaccgcgc gttcgcctgg cttacatggc ctgcattggc 480
54 atctgggtcc tggctttctt cttgagttcc ccatctctcg tcttccggga cacagccaac 540
56 ctgcattggaa aaatatccctg cttcaacaac ttccagctgt ccacacctgg gtcttcctcg 600
58 tggcccactc actcccaaattt ggaccctgtg gggtagatcc ggcacatgtt ggtgactgtc 660
60 acccgcttcc tctgtggctt cctgggtccca gtcctcatca tcacagctt ctacccacc 720
62 atcgtctgc aactgcagcg caaccgcctg gccaagacca agaagccctt caagatttt 780
64 gtgaccatca tcattacattt cttccctctgc tggtggccctt accacacactt caacccctta 840
66 gagctccacc acactgcccattt gcctggctct gtcttcagcc tgggtttggcc cctggccact 900
68 gcccttgcca ttgccaacag ctgcattgttccat ggtcaggactt 960
70 tcaagaagttt caaggtggcc ctcttccttc gcctggtcaa tgctctaagt gaagatacag 1020
72 gccactcttc ctaccccccattt catagaagct ttaccaagat gtcaatgaat gagaggactt 1080
74 ctatqaatqaa qaqggqagacc ggcattttt gaa 1112

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Input Set : A:\March'~1.txt
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79 <212> TYPE: PRT
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88 Pro Asp Tyr Leu Asp Ser Ile Val Val Leu Glu Asp Leu Ser Pro Leu
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92 Glu Ala Arg Val Thr Arg Ile Phe Leu Val Val Val Tyr Ser Ile Val
93           35          40          45
96 Cys Phe Leu Gly Ile Leu Gly Asn Gly Leu Val Ile Ile Ile Ala Thr
97           50          55          60
100 Phe Lys Met Lys Lys Thr Val Asn Met Val Trp Phe Leu Asn Leu Ala
101 65           70          75          80
104 Val Ala Asp Phe Leu Phe Asn Val Phe Leu Pro Ile His Ile Thr Tyr
105           85          90          95
108 Ala Ala Met Asp Tyr His Trp Val Phe Gly Thr Ala Met Cys Lys Ile
109           100         105         110
112 Ser Asn Phe Leu Leu Ile His Asn Met Phe Thr Ser Val Phe Leu Leu
113           115         120         125
116 Thr Ile Ile Ser Ser Asp Arg Cys Ile Ser Val Leu Leu Pro Val Trp
117           130         135         140
120 Ser Gln Asn His Arg Ser Val Arg Leu Ala Tyr Met Ala Cys Met Val
121 145           150         155         160
124 Ile Trp Val Leu Ala Phe Phe Leu Ser Ser Pro Ser Leu Val Phe Arg
125           165         170         175
128 Asp Thr Ala Asn Leu His Gly Lys Ile Ser Cys Phe Asn Asn Phe Ser
129           180         185         190
132 Leu Ser Thr Pro Gly Ser Ser Trp Pro Thr His Ser Gln Met Asp
133           195         200         205
136 Pro Val Gly Tyr Ser Arg His Met Val Val Thr Val Arg Phe Leu
137           210         215         220
140 Cys Gly Phe Leu Val Pro Val Leu Ile Ile Thr Ala Cys Tyr Leu Thr
141 225           230         235         240
144 Ile Val Cys Lys Leu Gln Arg Asn Arg Leu Ala Lys Thr Lys Pro
145           245         250         255
148 Phe Lys Ile Ile Val Thr Ile Ile Ile Thr Phe Phe Leu Cys Trp Cys
149           260         265         270
152 Pro Tyr His Thr Leu Asn Leu Leu Glu Leu His His Thr Ala Met Pro
153           275         280         285
156 Gly Ser Val Phe Ser Leu Gly Leu Pro Leu Ala Thr Ala Leu Ala Ile
157           290         295         300
160 Ala Asn Ser Cys Met Asn Pro Ile Leu Tyr Val Phe Met Gly Gln Asp
161 305           310         315         320
164 Phe Lys Lys Phe Lys Val Ala Leu Phe Ser Arg Leu Val Asn Ala Leu
165           325         330         335
168 Ser Glu Asp Thr Gly His Ser Ser Tyr Pro Ser His Arg Ser Phe Thr
169           340         345         350

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173 355 360 365
176 Gly Met Leu
177 370
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181 <211> LENGTH: 1116
182 <212> TYPE: DNA
183 <213> ORGANISM: Mus musculus
185 <400> SEQUENCE: 3
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188 ggctactttg tggacttggaa ggaggcgagt ccgtgggagg ccaagggtggc cccggcttcc 120
190 ctgggtgtga tctacagctt ggtgtgcttc ctgggtctcc taggcaacgg cctggtgatt 180
192 gtcatcgcca ctttcaagat gaagaagacc gtgaacactg tgggtttgt caacctggct 240
194 gtggccgact tcctgttcaa catcttttg ccgatgcaca tcacctaacc ggcacatggac 300
196 taccactggg tggtcgggaa ggccatgtgc aagatcagca acttcttgcact cagccacaac 360
198 atgtacacca ggcgtttccct gctgactgtc atcagctttg accgctgcat ctccgtgctg 420
200 ctccccgtct ggtcccagaa ccaccgcagc atcgcgctgg cctacatgac ctgctcgcc 480
202 gtctgggtcc tggctttctt cttgagctcc ccgtcccttgc tcttccggga caccgccaac 540
204 attcatggga agataaacctg cttaacaac ttcagcttgg ccgcgcctga gtcctccca 600
206 catccgcacc actcgcaagt agtttccaca gggtacagca gacacgtggc ggtcaactgtc 660
208 acccgcttcc ttgcggctt cctgatcccc gtcttcatca tcacggcctg ctaccttacc 720
210 atcgttccatca agctgcagcg caaccgcctg gccaagaaca agaaggccctt caagatcatc 780
212 atcaccatca tcatacacctt cttccctctgc tggtgcccctt accacaccctt ctacctgctg 840
214 gagctccacc acacagctgt gccaagctct gtcttcagcc tggggctacc cctggccacg 900
216 gccgtcgcca tcgccaacag ctgcatgaac cccattctgt acgtcttcat gggccacgac 960
218 ttcagaaaat tcaaggtggc cctcttctcc cgctggcca acgcccctgag tgaggacaca 1020
220 ggccttccctt cctaccccaag tcacaggagc ttccaccaaga tgtcgtctt gaatgagaag 1080
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226 <211> LENGTH: 371
227 <212> TYPE: PRT
228 <213> ORGANISM: Mus musculus
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240 Glu Ala Lys Val Ala Pro Val Phe Leu Val Val Ile Tyr Ser Leu Val
241 35 40 45
244 Cys Phe Leu Gly Leu Leu Gly Asn Gly Leu Val Ile Val Ile Ala Thr
245 50 55 60
248 Phe Lys Met Lys Lys Thr Val Asn Thr Val Trp Phe Val Asn Leu Ala
249 65 70 75 80
252 Val Ala Asp Phe Leu Phe Asn Ile Phe Leu Pro Met His Ile Thr Tyr
253 85 90 95
256 Ala Ala Met Asp Tyr His Trp Val Phe Gly Lys Ala Met Cys Lys Ile
257 100 105 110
260 Ser Asn Phe Leu Leu Ser His Asn Met Tyr Thr Ser Val Phe Leu Leu
261 115 120 125

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264 Thr Val Ile Ser Phe Asp Arg Cys Ile Ser Val Leu Leu Pro Val Trp
265 130 . 135 140
268 Ser Gln Asn His Arg Ser Ile Arg Leu Ala Tyr Met Thr Cys Ser Ala
269 145 150 155 160
272 Val Trp Val Leu Ala Phe Phe Leu Ser Ser Pro Ser Leu Val Phe Arg
273 165 170 175
276 Asp Thr Ala Asn Ile His Gly Lys Ile Thr Cys Phe Asn Asn Phe Ser
277 180 185 190
280 Leu Ala Ala Pro Glu Ser Ser Pro His Pro Ala His Ser Gln Val Val
281 195 200 205
284 Ser Thr Gly Tyr Ser Arg His Val Ala Val Thr Val Thr Arg Phe Leu
285 210 215 220
288 Cys Gly Phe Leu Ile Pro Val Phe Ile Ile Thr Ala Cys Tyr Leu Thr
289 225 230 235 240
292 Ile Val Phe Lys Leu Gln Arg Asn Arg Leu Ala Lys Asn Lys Lys Pro
293 245 250 255
296 Phe Lys Ile Ile Ile Thr Ile Ile Thr Phe Phe Leu Cys Trp Cys
297 260 265 270
300 Pro Tyr His Thr Leu Tyr Leu Leu Glu Leu His His Thr Ala Val Pro
301 275 280 285
304 Ser Ser Val Phe Ser Leu Gly Leu Pro Leu Ala Thr Ala Val Ala Ile
305 290 295 300
308 Ala Asn Ser Cys Met Asn Pro Ile Leu Tyr Val Phe Met Gly His Asp
309 305 310 315 320
312 Phe Arg Lys Phe Lys Val Ala Leu Phe Ser Arg Leu Ala Asn Ala Leu
313 325 330 335
316 Ser Glu Asp Thr Gly Pro Ser Ser Tyr Pro Ser His Arg Ser Phe Thr
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330 <212> TYPE: DNA
331 <213> ORGANISM: Rattus norvegicus
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338 ctgggtgttaa tctacagctt ggtgtgcttc ctggggatcc taggcaatgg cctggtgatt 180
340 gtcatcgcca cttcaagat gaagaagacg gtgaacacccg tgggtttgt caacctggcc 240
342 gtggctgact tcctgttcaa catcttcttg cccatccaca tcaccttatgc cgctatggac 300
344 taccactggg tgttcggaa agccatgtgc aagatttagta gcttctgct aagccacaac 360
346 atgtacacca gcgttccct gctcaactgtc atcagcttc accgctgcat ctccgtgctc 420
348 ctccccgtct ggtcccagaa ccaccgcagc gtgcgtctgg cctacatgac ctgcgtggtt 480
350 gtctgggtct ggctttcttc tgagtctccc ccgtccctcg tcttcggaca cgtcagcacc 540
352 agccacggga agataaacctg cttcaacaac ttccagcctgg cggcgccccga gcctttctct 600
354 cattccacccc acccgcgAAC agaccggta gggtagcagca gacatgtggc ggtcaccgtc 660
356 acccgcttcc tctgtggctt cctgatcccc gtcttcatca tcacggcctg ttacctcacc 720

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362	gagctccacc	acacggctgt	gccagcctct	gtcttcagcc	tgggactgcc	cctggccaca	900										
364	gccgtcgcca	tcgccaacag	ctgttatgaac	ccccatcctgt	acgtcttcat	ggggcacgac	960										
366	ttcaaaaaat	tcaaggtggc	cctttctcc	cgcctggta	atgcctgag	cgaggacaca	1020										
368	ggaccctcct	cctacccag	tcacaggagc	ttcacccaaga	tgtcctcatt	gattgagaag	1080										
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384	Ser	Asp	Gly	Ser	Asp	Tyr	Ile	Val	Asp	Leu	Glu	Ala	Gly	Pro	Leu		
385				20				25				30					
388	Glu	Ala	Lys	Val	Ala	Glu	Val	Phe	Leu	Val	Val	Ile	Tyr	Ser	Leu	Val	
389				35				40				45					
392	Cys	Phe	Leu	Gly	Ile	Leu	Gly	Asn	Gly	Leu	Val	Ile	Val	Ile	Ala	Thr	
393				50				55				60					
396	Phe	Lys	Met	Lys	Lys	Thr	Val	Asn	Thr	Val	Trp	Phe	Val	Asn	Leu	Ala	
397	65				70				75			80					
400	Val	Ala	Asp	Phe	Leu	Phe	Asn	Ile	Phe	Leu	Pro	Ile	His	Ile	Thr	Tyr	
401					85				90			95					
404	Ala	Ala	Met	Asp	Tyr	His	Trp	Val	Phe	Gly	Lys	Ala	Met	Cys	Lys	Ile	
405					100				105			110					
408	Ser	Ser	Phe	Leu	Leu	Ser	His	Asn	Met	Tyr	Thr	Ser	Val	Phe	Leu	Leu	
409					115				120			125					
412	Thr	Val	Ile	Ser	Phe	Asp	Arg	Cys	Ile	Ser	Val	Leu	Leu	Pro	Val	Trp	
413					130				135			140					
416	Ser	Gln	Asn	His	Arg	Ser	Val	Arg	Leu	Ala	Tyr	Met	Thr	Cys	Val	Val	
417	145					150				155			160				
420	Val	Trp	Val	Trp	Leu	Ser	Ser	Glu	Ser	Pro	Pro	Ser	Leu	Val	Phe	Gly	
421						165				170			175				
424	His	Val	Ser	Thr	Ser	His	Gly	Lys	Ile	Thr	Cys	Phe	Asn	Asn	Phe	Ser	
425						180				185			190				
428	Leu	Ala	Ala	Pro	Glu	Pro	Phe	Ser	His	Ser	Thr	His	Pro	Arg	Thr	Asp	
429					195				200			205					
432	Pro	Val	Gly	Tyr	Ser	Arg	His	Val	Ala	Val	Thr	Val	Thr	Arg	Phe	Leu	
433					210				215			220					
436	Cys	Gly	Phe	Leu	Ile	Pro	Val	Phe	Ile	Ile	Thr	Ala	Cys	Tyr	Leu	Thr	
437	225					230				235			240				
440	Ile	Val	Phe	Lys	Leu	Gln	Arg	Asn	Arg	Gln	Ala	Lys	Thr	Lys	Lys	Pro	
441						245				250			255				
444	Phe	Lys	Ile	Ile	Ile	Thr	Ile	Ile	Thr	Phe	Phe	Leu	Cys	Trp	Cys		
445						260				265			270				
448	Pro	Tyr	His	Thr	Leu	Tyr	Leu	Leu	Glu	Leu	His	His	Thr	Ala	Val	Pro	
449						275				280			285				
452	Ala	Ser	Val	Phe	Ser	Leu	Gly	Leu	Pro	Leu	Ala	Thr	Ala	Val	Ala	Ile	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/30/2005
PATENT APPLICATION: US/10/603,566A TIME: 10:56:08

Input Set : A:\March'~1.txt
Output Set: N:\CRF4\03302005\J603566A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:92; Xaa Pos. 3,4,5,7,9
Seq#:93; Xaa Pos. 4,5,7,9
Seq#:94; Xaa Pos. 1,2,3,4,5,6,7,8,9

VERIFICATION SUMMARY
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Input Set : A:\March'~1.txt
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L:1974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:92 after pos.:0
L:2012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93 after pos.:0
L:2062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:94 after pos.:0